

Met	Asp	Trp	Pro	His	Asn	Leu	Leu	Phe	Leu	Leu	Thr	Ile	Ser	Ile	1	5	10	15
Phe	Leu	Gly	Leu	Gly	Gln	Pro	Arg	Ser	Pro	Lys	Ser	Lys	Arg	Lys	20	25	30	
Gly	Gln	Gly	Arg	Pro	Gly	Pro	Leu	Ala	Pro	Gly	Pro	His	Gln	Val	35	40	45	
Pro	Leu	Asp	Leu	Val	Ser	Arg	Met	Lys	Pro	Tyr	Ala	Arg	Met	Glu	50	55	60	
Glu	Tyr	Glu	Arg	Asn	Ile	Glu	Glu	Met	Val	Ala	Gln	Leu	Arg	Asn	65	70	75	
Ser	Ser	Glu	Leu	Ala	Gln	Arg	Lys	Cys	Glu	Val	Asn	Leu	Gln	Leu	80	85	90	
Trp	Met	Ser	Asn	Lys	Arg	Ser	Leu	Ser	Pro	Trp	Gly	Tyr	Ser	Ile	95	100	105	
Asn	His	Asp	Pro	Ser	Arg	Ile	Pro	Val	Asp	Leu	Pro	Glu	Ala	Arg	110	115	120	
Cys	Leu	Cys	Leu	Gly	Cys	Val	Asn	Pro	Phe	Thr	Met	Gln	Glu	Asp	125	130	135	
Arg	Ser	Met	Val	Ser	Val	Pro	Val	Phe	Ser	Gln	Val	Pro	Val	Arg	140	145	150	
Arg	Arg	Leu	Cys	Pro	Pro	Pro	Pro	Arg	Thr	Gly	Pro	Cys	Arg	Gln	155	160	165	
Arg	Ala	Val	Met	Glu	Thr	Ile	Ala	Val	Gly	Cys	Thr	Cys	Ile	Phe	170	175	180	

FIGURE 1

aggcgggcag cagctgcagg ctgaccttgc agcttggcgg aatggactgg 50
 cctcacaacc tgctgtttct tcttaccatt tccatcttcc tggggctggg 100
 ccagcccagg agccccaaaa gcaagaggaa ggggcaaggg cggcctgggc 150
 ccctggcccc tggccctcac caggtgccac tggacctggt gtcacggatg 200
 aaaccgtatg cccgcatgga ggagtatgag aggaacatcg aggagatggt 250
 ggcccagctg aggaacagct cagagctggc ccagagaaaag tgtgaggtca 300
 acttgcagct gtggatgtcc aacaagagga gcctgtctcc ctggggctac 350
 agcatcaacc acgaccccag ccgtatcccc gtggacctgc cggaggcacg 400
 gtgcctgtgt ctgggctgtg tgaaccctt caccatgcag gaggaccgca 450
 gcatggtgag cgtgccggtg ttcagccagg ttctgtgcg ccgccgcctc 500
 tgcccgccac cgccccgcac agggccttgc cgccagcgcg cagtcatgga 550
 gaccatcgct gtgggctgca cctgcatctt ctgaatcacc tggcccagaa 600
 gccaggccag cagcccagaga ccacccctct tgcacctttg tgccaagaaa 650
 ggccatgaa aagtaaacac tgacttttga aagcaag 687

FIGURE 2

Met	Thr	Leu	Leu	Pro	Gly	Leu	Leu	Phe	Leu	Thr	Trp	Leu	His	Thr	1	5	10	15
Cys	Leu	Ala	His	His	Asp	Pro	Ser	Leu	Arg	Gly	His	Pro	His	Ser	20	25	30	
His	Gly	Thr	Pro	His	Cys	Tyr	Ser	Ala	Glu	Glu	Leu	Pro	Leu	Gly	35	40	45	
Gln	Ala	Pro	Pro	His	Leu	Leu	Ala	Arg	Gly	Ala	Lys	Trp	Gly	Gln	50	55	60	
Ala	Leu	Pro	Val	Ala	Leu	Val	Ser	Ser	Leu	Glu	Ala	Ala	Ser	His	65	70	75	
Arg	Gly	Arg	His	Glu	Arg	Pro	Ser	Ala	Thr	Thr	Gln	Cys	Pro	Val	80	85	90	
Leu	Arg	Pro	Glu	Glu	Val	Leu	Glu	Ala	Asp	Thr	His	Gln	Arg	Ser	95	100	105	
Ile	Ser	Pro	Trp	Arg	Tyr	Arg	Val	Asp	Thr	Asp	Glu	Asp	Arg	Tyr	110	115	120	
Pro	Gln	Lys	Leu	Ala	Phe	Ala	Glu	Cys	Leu	Cys	Arg	Gly	Cys	Ile	125	130	135	
Asp	Ala	Arg	Thr	Gly	Arg	Glu	Thr	Ala	Ala	Leu	Asn	Ser	Val	Arg	140	145	150	
Leu	Leu	Gln	Ser	Leu	Leu	Val	Leu	Arg	Arg	Arg	Pro	Cys	Ser	Arg	155	160	165	
Asp	Gly	Ser	Gly	Leu	Pro	Thr	Pro	Gly	Ala	Phe	Ala	Phe	His	Thr	170	175	180	
Glu	Phe	Ile	His	Val	Pro	Val	Gly	Cys	Thr	Cys	Val	Leu	Pro	Arg	185	190	195	
Ser	Val														197			

FIGURE 3

gccaggtgtg caggccgctc caagcccagc ctgccccgct gccgccacca 50
 tgacgctcct ccccggcctc ctgtttctga cctggctgca cacatgcctg 100
 gccaccatg acccctccct cagggggcac cccacagtc acggtacccc 150
 aactgctac tcggctgagg aactgccctt cggccaggcc cccccacacc 200
 tgctggctcg aggtgccaaag tgggggcagg ctttgctgtg agccctgggtg 250
 tccagcctgg aggcagcaag ccacaggggg aggcacgaga ggccctcagc 300
 tacgaccag tgcccgggtg tgccggccga ggaggtgttg gaggcagaca 350
 cccaccagcg ctccatctca ccttgagat accgtgtgga cacggatgag 400
 gaccgctatc cacagaagct ggccttcgcc gagtgcctgt gcagaggctg 450
 tatcgatgca cggacggggc gcgagacagc tgcgtcaac tccgtgcggc 500
 tgctccagag cctgctgggtg ctgcgccgcc ggccctgctc ccgcgacggc 550
 tcggggctcc ccacacctgg ggcctttgcc ttccacaccg agttcatcca 600
 cgtccccgtc ggctgcacct gcgtgctgcc ccgttcagtg tgaccgccga 650
 ggccgtgggg cccctagact ggacacgtgt gctccccaga gggcaccccc 700
 tatttatgtg tatttattgt tatttatatg cctcccccaa cactaccctt 750
 ggggtctggg cattccccgt gtctggagga cagcccccca ctgttctcct 800
 catctccagc ctcagtagtt gggggtagaa ggagctcagc acctcttcca 850
 gcccttaaag ctgcagaaaa ggtgtcacac ggctgcctgt accttggctc 900
 cctgtcctgc tcccggttc ccttacccta tcaactggcct caggccccgc 950
 aggtgcctc ttcccaacct ccttgaagt acccctgttt cttaaacaat 1000
 tatttaagtg tacgtgtatt attaaactga tgaacacatc cccaaaa 1047

FIGURE 4

ggcagcaggg accaagagag gcacgcttgc ccttttatga catcagagct 50
 cctggttctt gctccttggg actctgggac ttacaccagt ggcacccctg 100
 gctcnnnnnn nnnnnaattc ggtacgaggc tgggggttcag gcgggcagca 150
 gctgcaggct gaccttgcag cttggcgga tggactggcc tcacaacctg 200
 ctgtttcttc ttaccatttc catcttcctg gggtctgggc agcccaggag 250
 ccccaaaagc aagaggaagg ggcaagggcg gcctgggccc ctggtccttg 300
 gccctcacca ggtgccactg gacctggtgt cacggatgaa accgtatgcc 350
 cgcattggagg agtatgagag gaacatcgag gagatgttgg cccagctgag 400
 gaacagttca gagctggccc agagaaagtg tgagggtcaac ttgcagctgt 450
 ggatgtccaa caagaggagc ctgtctccct ggggctacag catcaaccac 500
 gaccccagcc gtatccccgt ggacctccgg aggcacggtg cctgtgtctg 550
 ggcttgtgtg aacccttca ccatgcagga ggaccgcagc atgggtgagcg 600
 tgccggtgtt cagccaggtt cctgtgcgcc gccgcctctg cccgccaccg 650
 cccgcacag ggccttgccg ccagcgcgca gtcattggaga ccatcgctgt 700
 gggctgcacc tgcattcttc gaatcgacct ggcccagaag ccaggccagc 750
 agcccgagac catctcctt gcacctttgt gcccaagaaag gcctatgaaa 800
 agtaaact gacttttgaa agcaaaaaaa 830

FIGURE 5


```

1  . . . . . MIPGKTSLVSLLLLL
1  . . . . . MDWPHNLLFLTISIFLGLGQPRSPKSKRKGGQGRPPGLAPGP
1  MTLPLGLFLTWLHTCLAHHDPSSLRGCHPHSHGTPHCYSAEELPLGQAPPH

16  SLEAIVKAGITIPRNPGPCPNSEDKNFPR*TVMVNLNIHNRNTNTNPKRSSD
43  HQVPLDLVSRMKPYARMEEYE*RNI*EEMVAQLRN*SSELAQRKKEVNLQLWM
51  LARGAKWGQALPV*ALVSSLEAASHRG*RHERPSATTQCPVLRPEEVLEAD

66  YYNRS*TS*SPWNLH*RNE*DPIERYPSV*IWEAK*CRHLGCINADGNVDYHMNSVPI
93  SNKRS*LSPWGY*YSIN*HDPS*RIPVD*LPEARCLCLGCVNPF*MQE*DRSMVSVIP
101 THQRS*IS*SPWRVYRVDT*DED*RY*PQKLLAF*AECLCRGCIDART*GR*ETAA*LN*SVR

116 QQEI*L*VLRRE*PH*CPNS*. . . . .ERLEK*LV*SVGCTCYT*BIVHHVA
143 VFSQVPVRRRL. . . . .CPPPPT. . . . .GPCRQ*RAVMETIAVGC*TQIF. . . . .
151 LQSL*LV*RR*RP. . . . .CSR*DGSG*LP*T*PGAF*AEHT*EF*HV*PG*CT*CVL*BRSV. . .

```

FIGURE 7A

Tue Apr 27 16:58:30 1999
/home/ruby/va/Molbio/carpanda/temp/aa.out

```
59294  1 M D W P H N L L F L L T I S I F L G L G Q P R S P K S K R K G Q G R P G P L A P G P - - - H Q V P L
62377  1 M T L L P G L L F L T W L H T C L A H H D P - S L R G H P H S H G T P H C Y S A E E L P L G Q A P P

59294  48 D L V S R M K P Y A R M - - E E Y E R N I E E M V A Q L R N S S E L A Q R K C E V - - - N L Q L W
62377  50 H L L A R G A K W G Q A L P V A L V S S L E A A S H R G R H E R P S A T T Q C P V L R P E E V L E A

59294  92 M S N K R S L S P W G Y S I N H D P S R I P V D L P E A R C L C L G C V N P F T M Q E D R S M V S V
62377 100 D T H Q R S I S P W R Y R V D T D E D R Y P Q K L A F A E C L C R G C I D A R T G R E T A A L N S V

59294 142 P V F - S Q V P V R R R L C P P P - - - P R T G P C R Q R A V M E T I A V G C T C I F
62377 150 R L L Q S L L V L R R R P C S R D G S G L P T P G A F A F H T E F I H V P V G C T C V L P R S V
```

FIGURE 7B

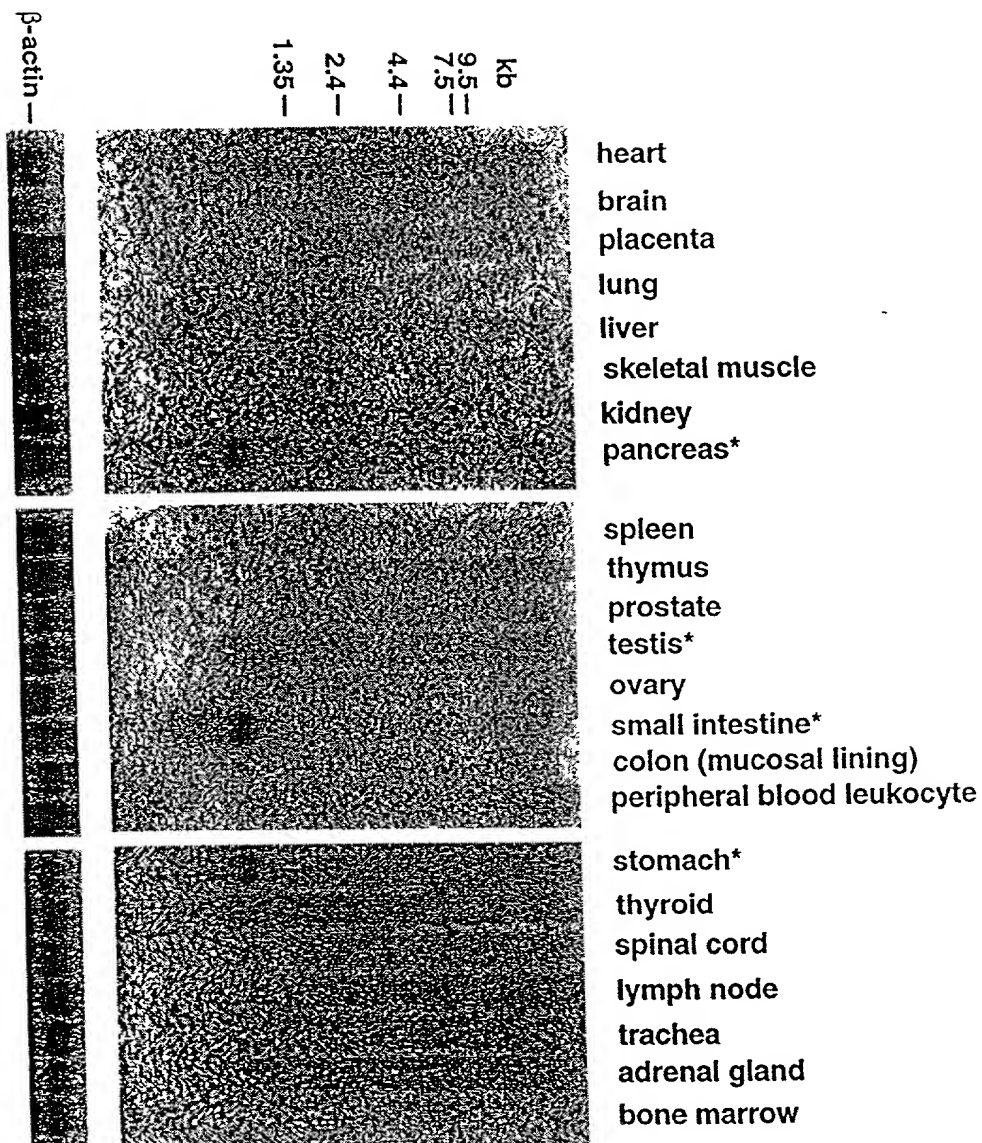
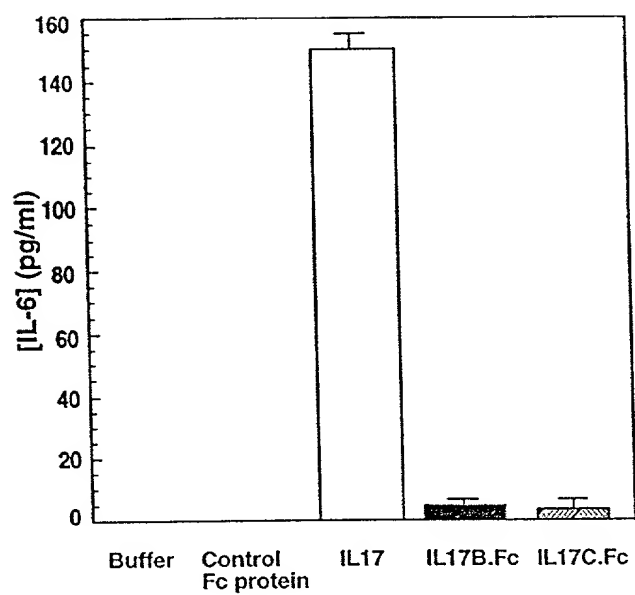


FIGURE 8

A. HFF cells



B. THP1 cells

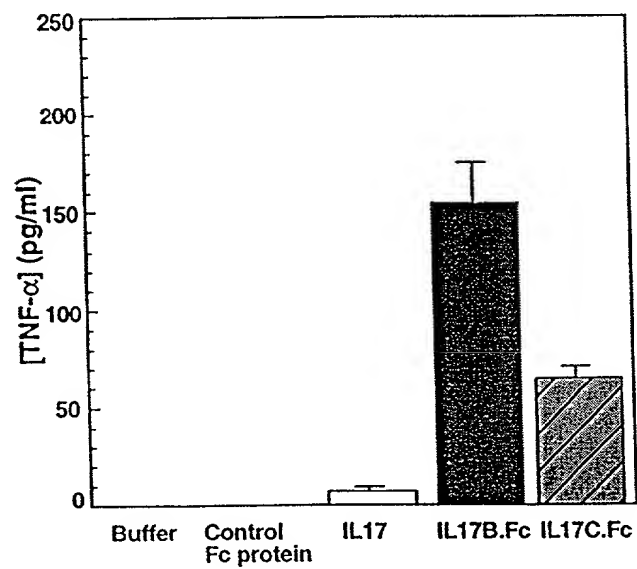
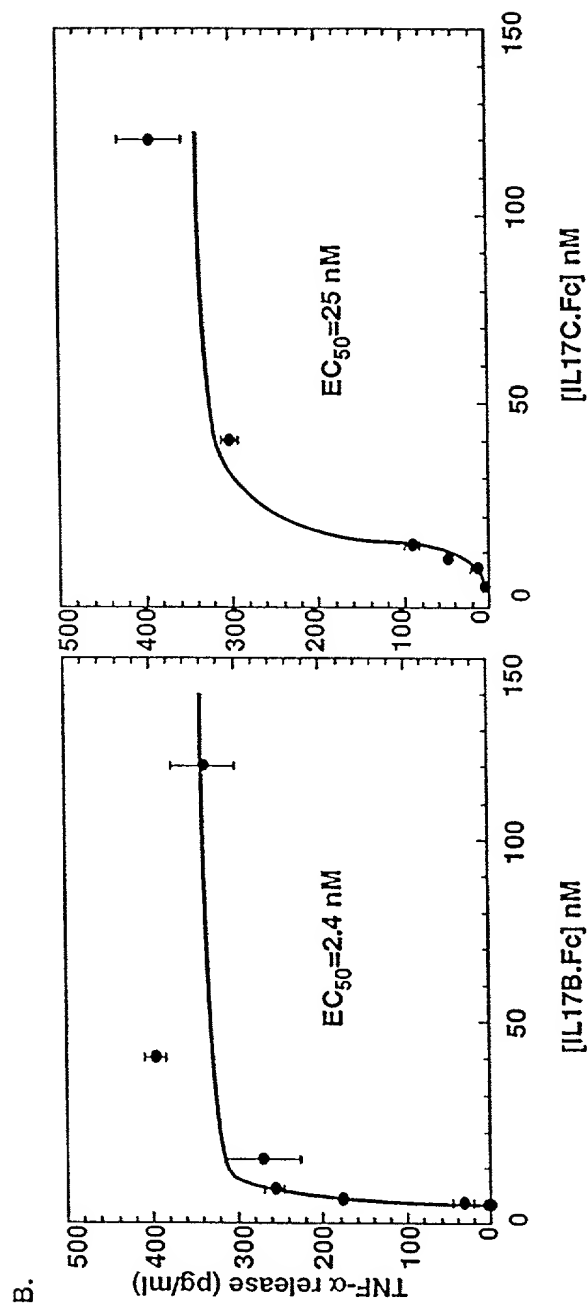
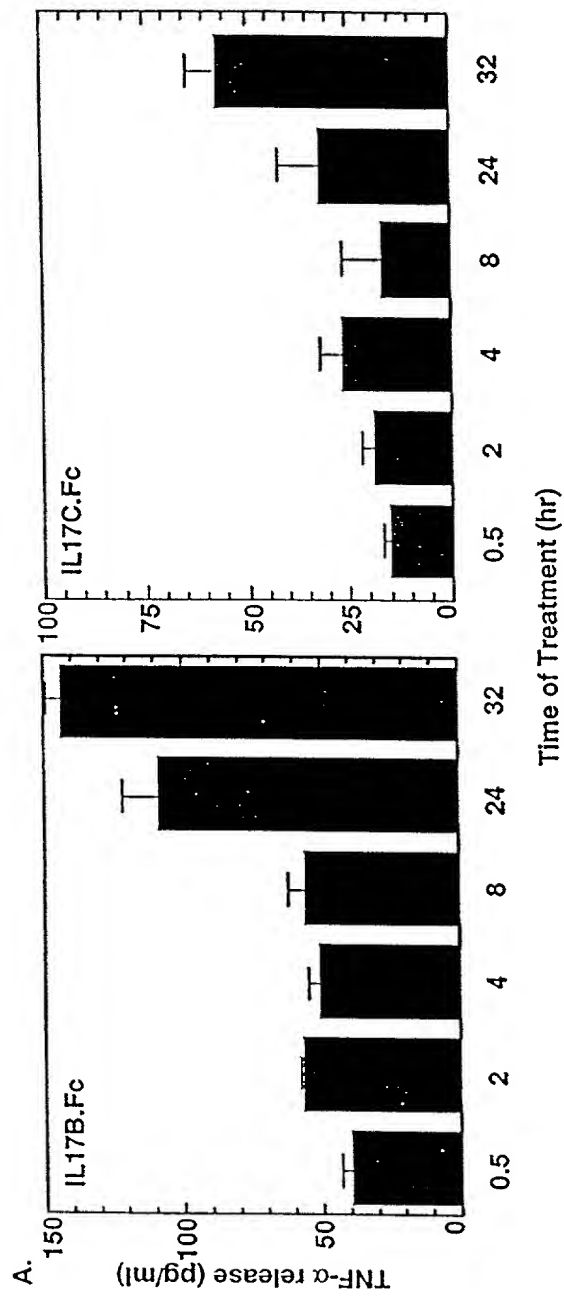


FIGURE 9

FIGURE 10
continued



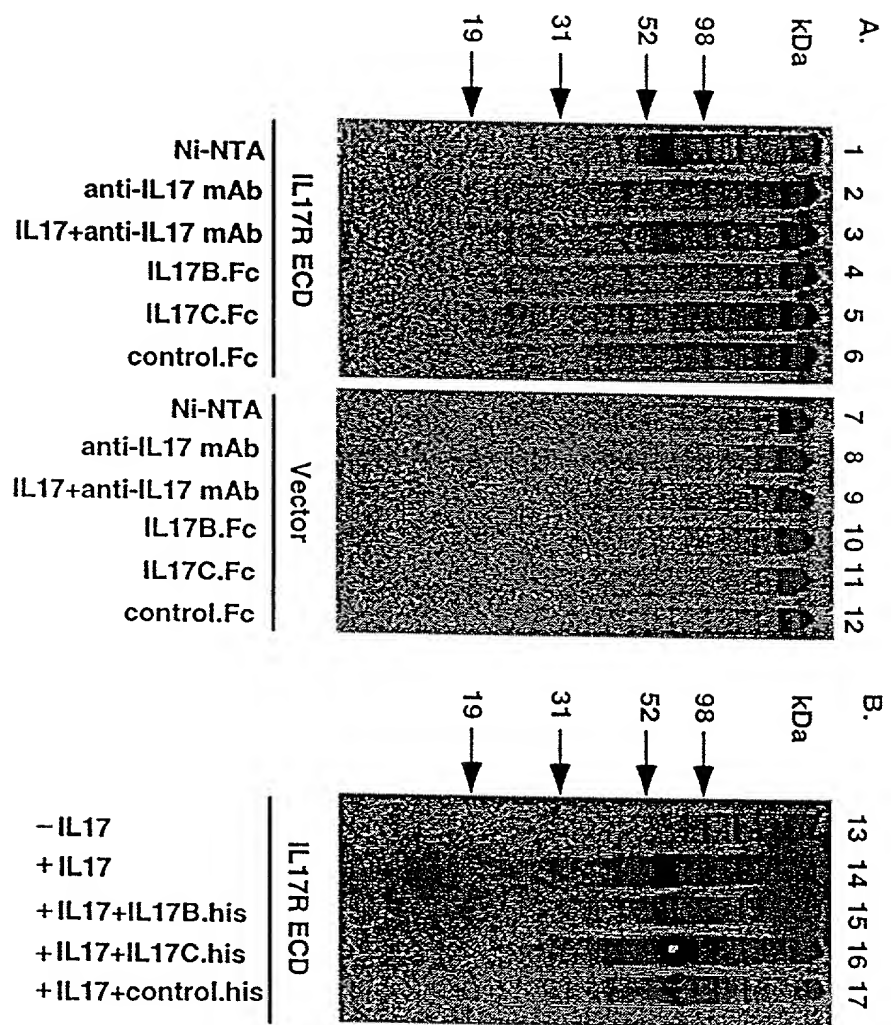


FIGURE 11

09854300 05 4 004

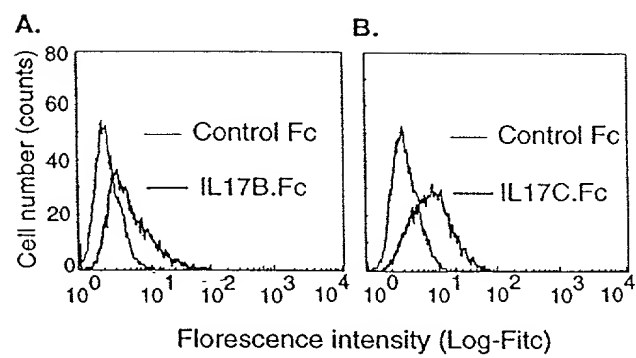


FIGURE 12

IL-17 induces breakdown and inhibits synthesis of cartilage matrix

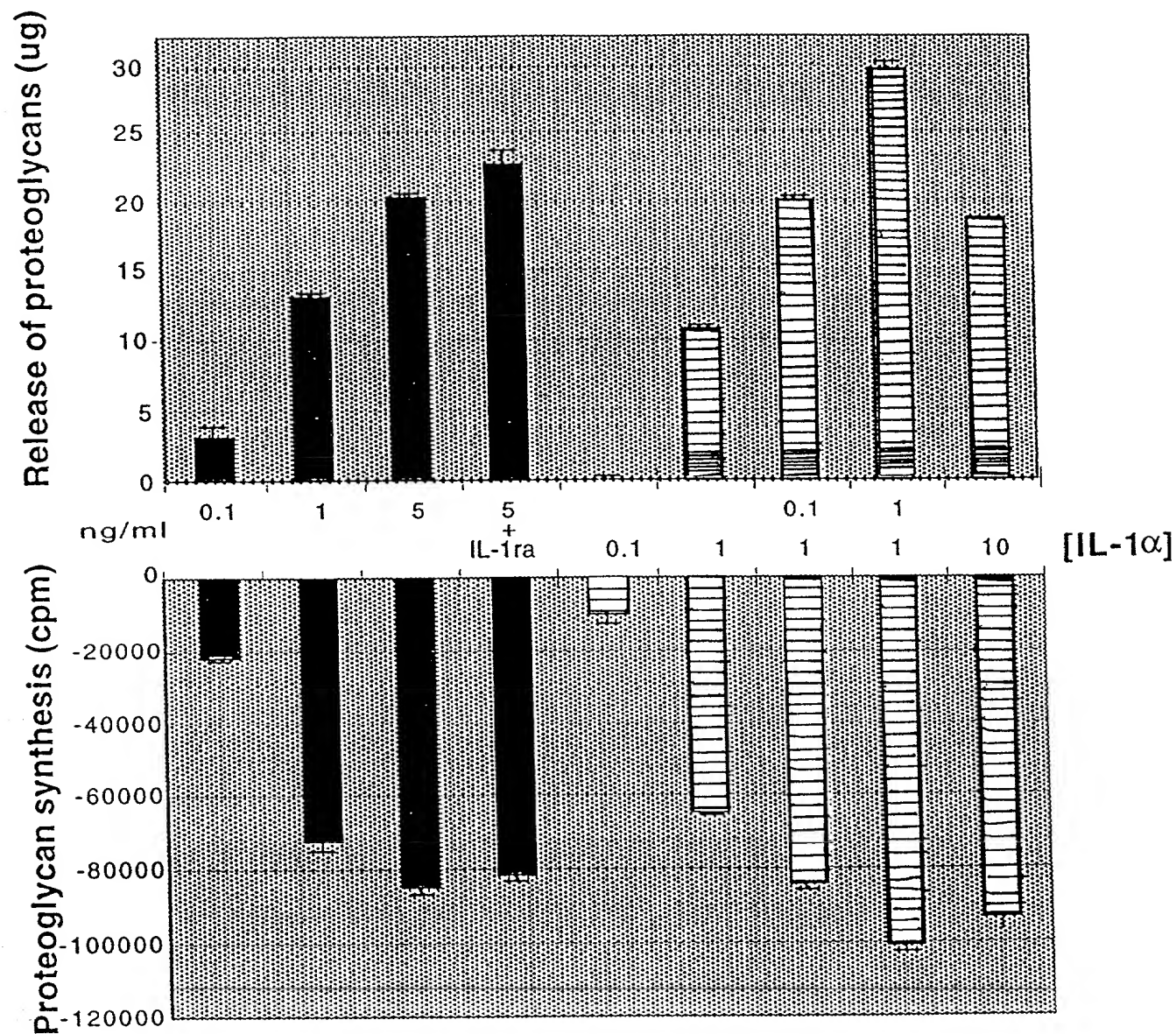


FIGURE 13

IL 17 increases basal and
IL-1 α -induced nitric oxide release

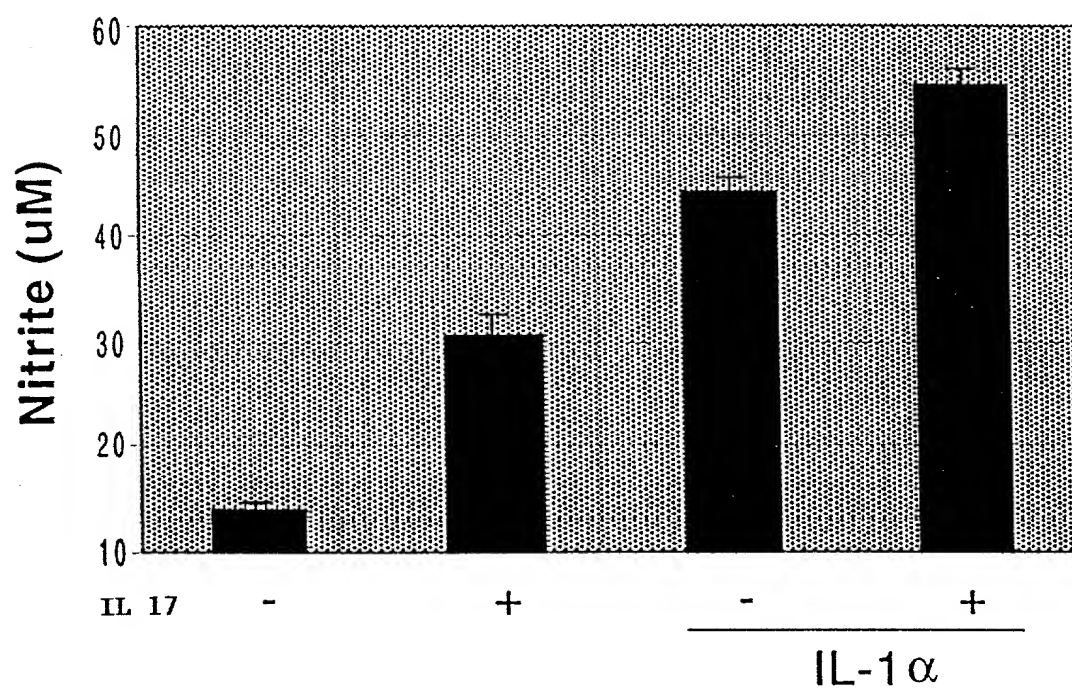
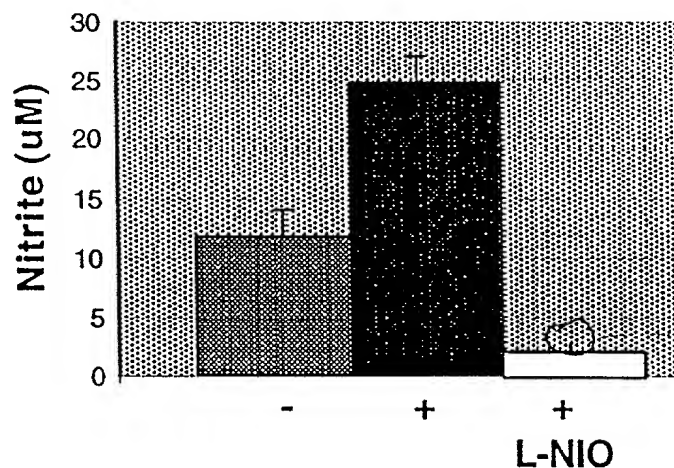


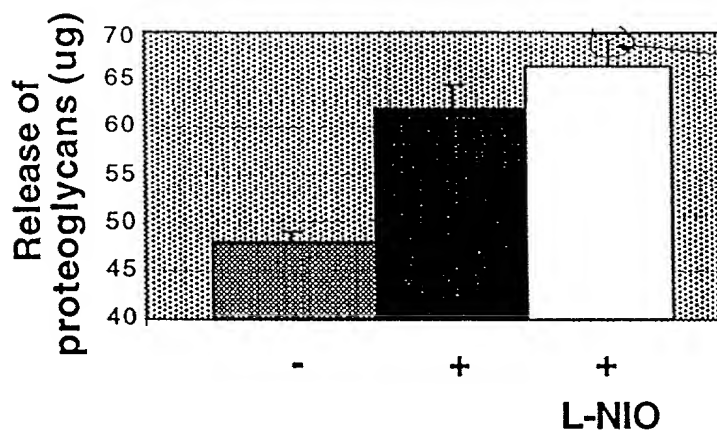
FIGURE 14

Inhibition of nitric oxide release does not block the detrimental effects of IL 17 on matrix breakdown or synthesis

A.



B.



C.

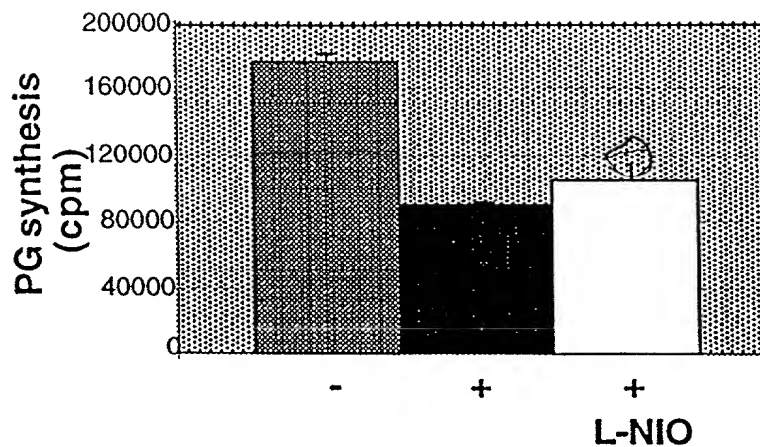


FIGURE 15

INHIBITION of NO release enhances
 IL-1- α -induced matrix breakdown
 but not matrix synthesis

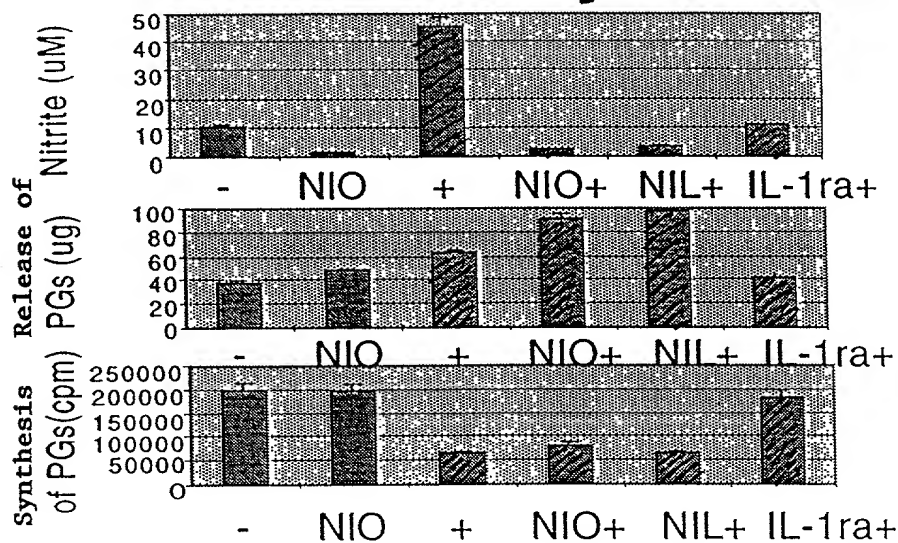


FIGURE 16

IL 17 homologue 1 (UNQ516)
has positive effects on
articular cartilage

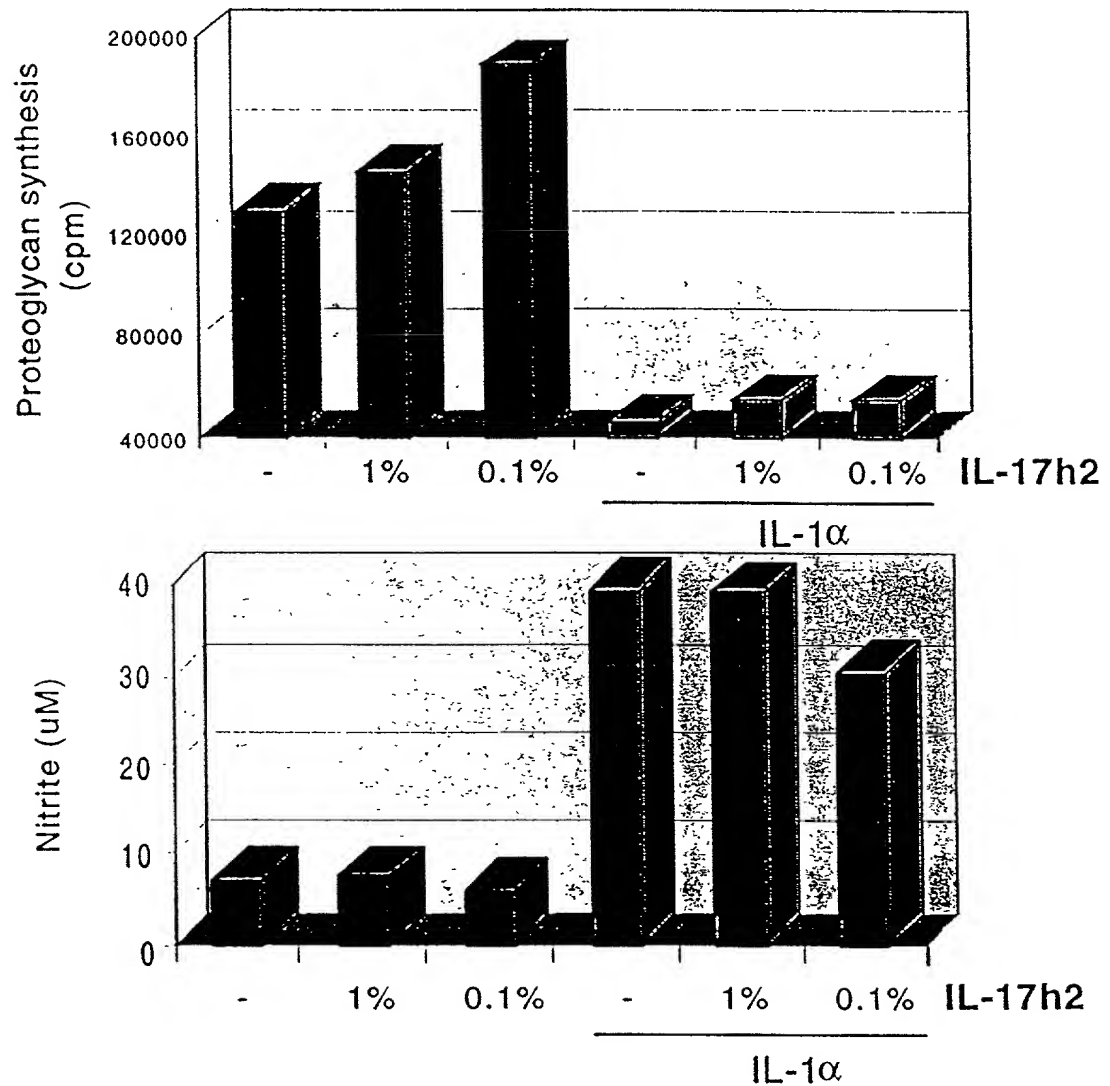


FIGURE 17

IL 17 homologue (UNQ 561) has detrimental effects on articular cartilage

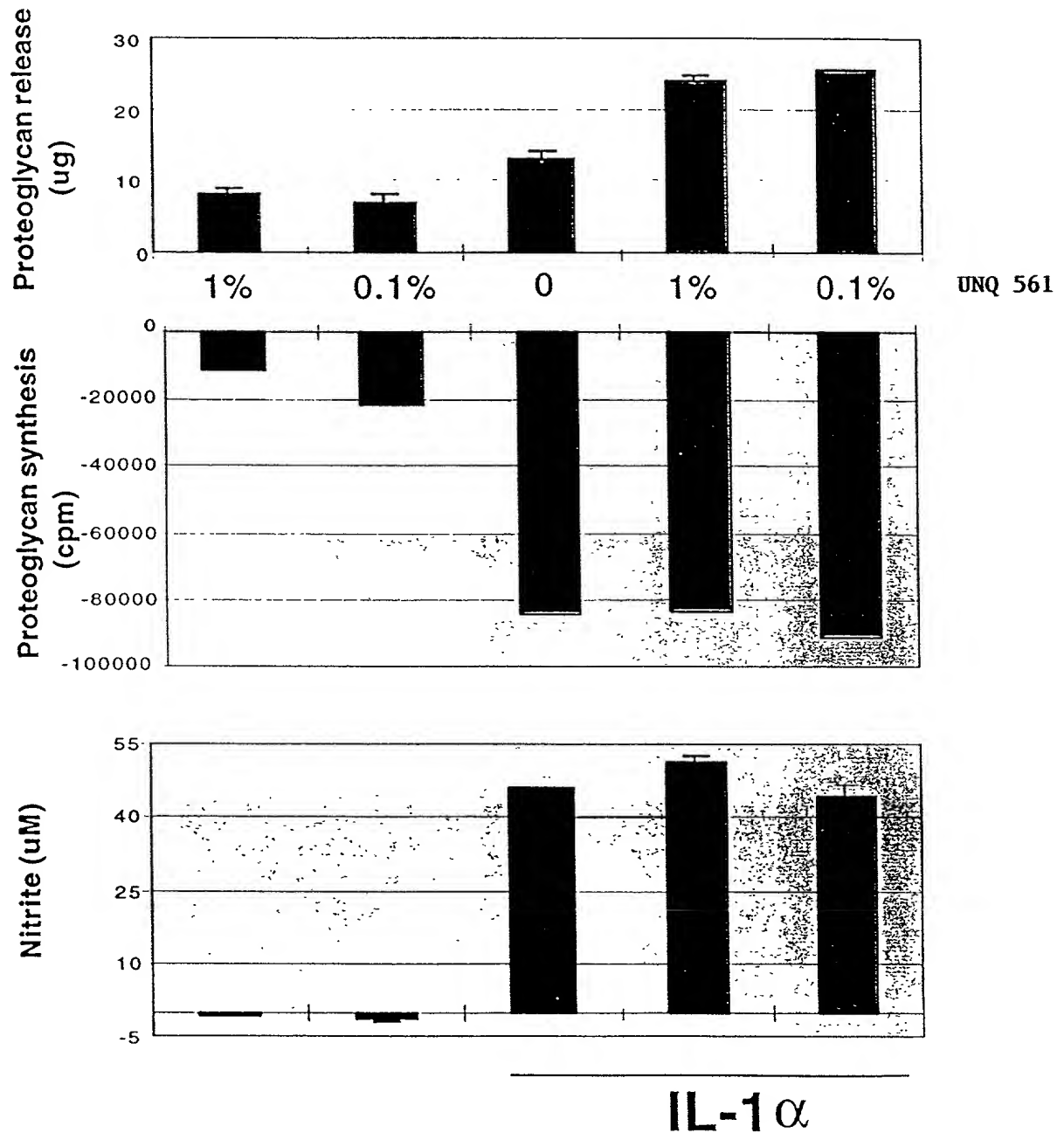


FIGURE 18